

sequence  
SEQUENCE LISTING

<110> Langley, Ries  
Fraser, John David

<120> Set 1 Proteins And Uses Thereof

<130> 55502-012us1

<140> 10/594,291

<141> 2004-12-07

<150> AU 2004901570

<151> 2004-03-24

<160> 18

<170> PatentIn version 3.5

<210> 1

<211> 231

<212> PRT

<213> Staphylococcus aureus

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20 25 30

Lys Gln Glu Arg Val Gln His Leu His Asp Ile Arg Asp Leu His Arg  
35 40 45

Tyr Tyr Ser Ser Glu Ser Phe Glu Tyr Ser Asn Val Ser Gly Lys Val  
50 55 60

Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Pro Lys Asp Gln  
65 70 75 80

Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Glu Gln Tyr Lys Glu  
85 90 95

Gly Leu Gln Gly Gln Asn Val Phe Val Val Gln Glu Leu Ile Asp Pro  
100 105 110

Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys  
115 120 125

Thr Ser Glu Thr Asn Thr Pro Leu Phe Val Asn Lys Val Asn Gly Glu  
130 135 140

Asp Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Gln Lys Glu Glu Ile  
Page 1

sequence															
145				150				155				160			
Ser	Leu	Lys	Glu	Leu <sub>165</sub>	Asp	Phe	Lys	Ile	Arg <sub>170</sub>	Gln	Gln	Leu	Val	Asn <sub>175</sub>	Asn
Tyr	Gly	Leu	Tyr <sub>180</sub>	Lys	Gly	Thr	Ser	Lys <sub>185</sub>	Tyr	Gly	Lys	Ile	Ile <sub>190</sub>	Ile	Asn
Leu	Lys	Asp <sub>195</sub>	Glu	Asn	Lys	Val	Glu <sub>200</sub>	Ile	Asp	Leu	Gly	Asp <sub>205</sub>	Lys	Leu	Gln
Phe	Glu <sub>210</sub>	Arg	Met	Gly	Asp	Val <sub>215</sub>	Leu	Asn	Ser	Lys	Asp <sub>220</sub>	Ile	Arg	Gly	Ile
Ser <sub>225</sub>	Val	Thr	Ile	Asn	Gln <sub>230</sub>	Ile									

Met	Lys	Leu	Lys	Thr	Leu	Ala	Lys	Ala	Thr	Leu	Ala	Leu	Gly	Leu	Leu	
1				5					10					15		
Thr	Thr	Gly	Val	Ile	Thr	Ser	Glu	Gly	Gln	Ala	Val	Gln	Ala	Ala	Glu	
			20					25					30			
Lys	Gln	Glu	Arg	Val	Gln	His	Leu	His	Asp	Ile	Arg	Asp	Leu	His	Arg	
		35					40					45				
Tyr	Tyr	Ser	Ser	Glu	Ser	Phe	Glu	Tyr	Ser	Asn	Val	Ser	Gly	Lys	Val	
	50					55					60					
Glu	Asn	Tyr	Asn	Gly	Ser	Asn	Val	Val	Arg	Phe	Asn	Pro	Lys	Asp	Gln	
65					70					75					80	
Asn	His	Gln	Leu	Phe	Leu	Leu	Gly	Lys	Asp	Lys	Glu	Gln	Tyr	Lys	Glu	
				85					90					95		
Gly	Leu	Gln	Gly	Gln	Asn	Val	Phe	Val	Val	Gln	Glu	Leu	Ile	Asp	Pro	
			100					105					110			
Asn	Gly	Arg	Leu	Ser	Thr	Val	Gly	Gly	Val	Thr	Lys	Lys	Asn	Asn	Lys	
		115					120					125				
Thr	Ser	Glu	Thr	Asn	Thr	Pro	Leu	Phe	Val	Asn	Lys	Val	Asn	Gly	Glu	



sequence

115	120	125
Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr Gly Gly		
130	135	140
Asn Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Asn Lys Glu Glu Val		
145	150	155 160
Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Gln Leu Val Glu Lys		
165	170	175
Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr Ile Asn		
180	185	190
Leu Lys Asp Glu Lys Lys Glu Val Ile Asp Leu Gly Asp Lys Leu Gln		
195	200	205
Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln Asn Ile		
210	215	220
Ala Val Thr Ile Asn Gln Ile		
225	230	

<210> 4  
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 <212> PRT  
 <213> Staphylococcus aureus

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Thr Thr Gly Val Ile Thr Ser Glu Gly Gln Ala Val His Ala Lys Glu
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Lys Gln Glu Arg Val Gln Glu Leu Tyr Asp Ile Lys Asp Leu Tyr Arg
35 40 45
Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly Lys Val
50 55 60
Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu Lys Gln
65 70 75 80
Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Asp Lys Tyr Lys Lys
85 90 95
Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile Asp Pro

sequence

100	105	110
Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys	115	120
Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr Gly Gly	130	135
Asn Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Asn Lys Glu Glu Val	145	150
Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Gln Leu Val Glu Lys	165	170
Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr Ile Asn	180	185
Leu Lys Asp Glu Lys Lys Glu Val Ile Asp Leu Gly Asp Lys Leu Gln	195	200
Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln Asn Ile	210	215
Ala Val Thr Ile Asn Gln Ile	225	230

<210> 5  
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Lys Gln Glu Arg Val Gln His Leu Tyr Asp Ile Lys Asp Leu His Arg	35	40	45	
Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly Lys Val	50	55	60	
Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu Asn Gln	65	70	75	80

Asn His Gln Leu Phe Leu Ser Gly Lys Asp Lys Asp Lys Tyr Lys Glu

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															sequence									
85										90					95									
Asn	Gln	Ser	Ser	Glu	Thr	Asn	Ile	His	Leu	Leu	Val	Asn	Lys	Leu	Asp									
			100				105						110											
Gly	Gly	Asn	Leu	Asp	Ala	Thr	Asn	Asp	Ser	Phe	Leu	Ile	Asn	Lys	Glu									
			115				120						125											
Glu	Val	Ser	Leu	Lys	Glu	Leu	Asp	Phe	Lys	Ile	Arg	Lys	Gln	Leu	Val									
		130				135					140													
Glu	Lys	Tyr	Gly	Leu	Tyr	Gln	Gly	Thr	Ser	Lys	Tyr	Gly	Lys	Ile	Thr									
145					150					155		160												
Ile	Ile	Leu	Asn	Gly	Gly	Lys	Lys	Gln	Glu	Ile	Asp	Leu	Gly	Asp	Lys									
			165							170					175									
Leu	Gln	Phe	Glu	Arg	Met	Gly	Asp	Val	Leu	Asn	Ser	Lys	Asp	Ile	Asn									
			180				185						190											
Lys	Ile	Glu	Val	Thr	Leu	Lys	Gln	Ile																
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<210> 8  
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 <213> Staphylococcus aureus

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catgatatta gagatttaca tcgatactac tcatcagaaa gtttcgaata tagtaatggt	180
agtggtaagg ttgaaaacta caatggttct aacgttgtac gctttaaccc aaaagatcaa	240
aatcaccaat tattcttatt aggaaaagat aaagaacaat ataaagaagg tctacaaggc	300
caaaatgtct ttgtagtaca agaattaatt gatccaaacg gcagactatc tactgttggt	360
ggtgtaacga agaaaaacaa caaaacttct gaaactaata cacctttatt tgtaataaaa	420
gttaatggtg aagattttaga tgcattcaatt gactcatttt taatccaaaa agaagaaatc	480
tcattaaaag agcttgattt caaaattaga caacaattag ttaataatta cggattatat	540
aaaggtacat ctaaatacgg taaaatcatt atcaatttga aagacgaaaa taaagtagaa	600
attgatttag gtgataaatt acaattcgag cgcattggcg atgtgttgaa tagtaaagac	660
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sequence

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 tatgatatta aagacttata tcgatactac tcatcagaaa gttttgaatt cagtaatatt 180  
 agtggttaagg ttgaaaacta taacggttct aacgttgtac gctttaacca agaaaaacaa 240  
 aatcaccaat tattcttatt aggaaaagat aaagataaat ataaaaaagg ccttgaaggc 300  
 cagaatgtct ttgtggtaaa agaattaatt gatccaaacg gtagactatc tactgttggt 360  
 ggtgtgacta agaaaaataa caaatcttct gaaactaata cacatttatt tgttaataaa 420  
 gtgtatggcg gaaatttaga tgcatacaatt gactcatttt taattaataa agaagaagtt 480  
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 agtggttaagg ttgaaaacta taacggttct aacgttgtac gctttaacca agaaaaacaa 240  
 aatcaccaat tattcttatt aggaaaagat aaagataaat ataaaaaagg ccttgaaggc 300  
 cagaatgtct ttgtggtaaa agaattaatt gatccaaacg gtagactatc tactgttggt 360  
 ggtgtgacta agaaaaataa caaatcttct gaaactaata cacatttatt tgttaataaa 420  
 gtgtatggcg gaaatttaga tgcatacaatt gactcatttt taattaataa agaagaagtt 480  
 tcaactgaaag aacttgattt caaaattaga aagcaattag ttgaaaaata tggtttatat 540  
 aaaggtacga ctaaatacgg taagatcact atcaatttga aagacgagaa aaaggaagta 600  
 attgatttag gtgataaact gcaattcgag cgcatgggtg atgtgttgaa tagtaaggat 660  
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aatcaccaat tattcttattc aggaaaagat aaagataaat ataaagaagg ccttgaaggc 300  
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ggtgtaacga agaaaaataa ccaatcttct gaaactaata cacctttatt tataaaaaaa 420  
gtgtatggcg gaaatttaga tgcattcaatt gaattcatttt taattaataa agaagaagtt 480  
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aacgttggtc gtttcaacca ggaaaaacag aaccaccagc tgttcctgct ggggtgaagac 180  
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gacccgaacg gtcgtctgtc caccgttggt ggtgttacca aaaaaaaca ccagtcctcc 300  
gaaaccaaca tccacctgct gggttaacaaa ctggacggtg gtaacctgga cgctaccaac 360  
gactccttcc tgatcaacaa agaagaagtt tccctgaaag aactggactt caaaatccgt 420  
aaacagctgg ttgaaaaata cggctctgtac cagggtacct ccaaatacgg taaaatcacc 480  
atcatcctga acggtggtaa aaaacaggaa atcgacctgg gtgacaaact gcagttcgaa 540  
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atctaa 606

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aacgttgttc gtttcaacca ggaaaaacag aaccaccagc tgttcctgct ggggtgaagac 180  
aaagctaaat acaaacaggg tctgcagggc caggacgttt tcgttggttaa agaactgac 240  
gacccgaacg gtcgtctgtc caccgttggt ggtgtttacca aaaaaaacia ccagtcctcc 300  
gaaaccaaca tccacctgct gggttaacaaa ctggacgggtg gtaacctgga cgctaccaac 360  
gactccttcc tgatcaacaa agaagaagtt tccctgaaag aactggactt caaaatccgt 420  
aaacagctgg ttgaaaaata cggctctgtac cagggtacct ccaaatacgg taaaatcacc 480  
atcatcctga acggtggtaa aaaacaggaa atcgacctgg gtgacaaact gcagttcgaa 540  
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Lys Val Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu  
35 40 45  
Asn Gln Asn His Gln Leu Phe Leu Ser Gly Lys Asp Lys Asp Lys Tyr  
50 55 60  
Lys Glu Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile  
65 70 75 80  
Asp Pro Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn  
85 90 95  
Asn Gln Ser Ser Glu Thr Asn Thr Pro Leu Phe Ile Lys Lys Val Tyr  
100 105 110  
Gly Gly Asn Leu Asp Ala Ser Ile Glu Ser Phe Leu Ile Asn Lys Glu  
115 120 125

sequence

Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln His Leu Val  
130 135 140

Lys Asn Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr  
145 150 155 160

Phe Asn Leu Lys Asp Gly Glu Lys Gln Glu Ile Asp Leu Gly Asp Lys  
165 170 175

Leu Gln Phe Glu His Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln  
180 185 190

Asn Ile Ala Val Thr Ile Asn Gln Ile  
195 200

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His Arg Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly  
20 25 30

Lys Val Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu  
35 40 45

Asn Gln Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Glu Lys Tyr  
50 55 60

Lys Glu Gly Ile Glu Gly Lys Asp Val Phe Val Val Lys Glu Leu Ile  
65 70 75 80

Asp Pro Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn  
85 90 95

Asn Lys Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr  
100 105 110

Gly Gly Asn Leu Asp Ala Ser Ile Asp Ser Phe Ser Ile Asn Lys Glu  
115 120 125

Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln His Leu Val  
130 135 140

sequence

Lys Asn Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr  
145 150 155 160

Ile Asn Leu Lys Asp Gly Glu Lys Gln Glu Ile Asp Leu Gly Asp Lys  
165 170 175

Leu Gln Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Asn  
180 185 190

Lys Ile Glu Val Thr Leu Lys Gln Ile  
195 200

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Tyr Arg Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly  
20 25 30

Lys Val Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu  
35 40 45

Lys Gln Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Asp Lys Tyr  
50 55 60

Lys Lys Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile  
65 70 75 80

Asp Pro Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn  
85 90 95

Asn Lys Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr  
100 105 110

Gly Gly Asn Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Asn Lys Glu  
115 120 125

Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Gln Leu Val  
130 135 140

Glu Lys Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr  
145 150 155 160

sequence  
 Ile Asn Leu Lys Asp Glu Lys Lys Glu Val Ile Asp Leu Gly Asp Lys  
 165 170 175

Leu Gln Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln  
 180 185 190

Asn Ile Ala Val Thr Ile Asn Gln Ile  
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Tyr Arg Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly  
 20 25 30

Lys Val Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu  
 35 40 45

Lys Gln Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Asp Lys Tyr  
 50 55 60

Lys Lys Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile  
 65 70 75 80

Asp Pro Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn  
 85 90 95

Asn Lys Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr  
 100 105 110

Gly Gly Asn Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Asn Lys Glu  
 115 120 125

Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Gln Leu Val  
 130 135 140

Glu Lys Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr  
 145 150 155 160

Ile Asn Leu Lys Asp Glu Lys Lys Glu Val Ile Asp Leu Gly Asp Lys  
 165 170 175

sequence

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180 185 190

Asn Ile Ala Val Thr Ile Asn Gln Ile  
195 200

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<213> Staphylococcus aureus

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His Arg Tyr Tyr Ser Ser Glu Ser Phe Glu Tyr Ser Asn Val Ser Gly  
20 25 30

Lys Val Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Pro Lys  
35 40 45

Asp Gln Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Glu Gln Tyr  
50 55 60

Lys Glu Gly Leu Gln Gly Gln Asn Val Phe Val Val Gln Glu Leu Ile  
65 70 75 80

Asp Pro Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn  
85 90 95

Asn Lys Thr Ser Glu Thr Asn Thr Pro Leu Phe Val Asn Lys Val Asn  
100 105 110

Gly Glu Asp Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Gln Lys Glu  
115 120 125

Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln Gln Leu Val  
130 135 140

Asn Asn Tyr Gly Leu Tyr Lys Gly Thr Ser Lys Tyr Gly Lys Ile Ile  
145 150 155 160

Ile Asn Leu Lys Asp Glu Asn Lys Val Glu Ile Asp Leu Gly Asp Lys  
165 170 175

Leu Gln Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Arg  
180 185 190

Gly Ile Ser Val Thr Ile Asn Gln Ile sequence  
195 200